SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: SmithKline Beecham plc et al

(ii) TITLE OF THE INVENTION: Novel compounds

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: SmithKline Beecham
  (B) STREET: Two, New Horizons Court, Great West Road
  (C) CITY: Brentford
  (D) STATE:
  (E) COUNTRY: UK
  (F) ZIP: TW8 9EP

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Valentine, Jill B
  (B) REGISTRATION NUMBER:
  (C) REFERENCE/DOCKET NUMBER: P31731

```
    (ix) TELECOMMUNICATION INFORMATION:
      (A)  TELEPHONE: 0181-9752000
      (B)  TELEFAX: 0181-9756294
      (C)  TELEX:



      (2) INFORMATION FOR SEQ ID NO:1:

    (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 7193 base pairs
      (B)  TYPE: nucleic acid
      (C)  STRANDEDNESS: single
      (D)  TOPOLOGY: linear


    (ii) MOLECULE TYPE: Other

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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CCATGGCGGG CGGCGGCTGC CCCGGAGCCT CGGCCGGACC GGTGACCAGG ACCACCCCGG     60
TGGGATAGTG GCCCGCCACC CGGCGCAGCA GACTCCCGGA CACGGACCCG TGGGTGTGCG    120
CGGAAAGGCC CGGAGGCCGG GTCACAGCCA CGGGTAACGC GCGGTGTCCT TGCCCGCGTA    180
ATCGGGGTCC AGATAGACGA AGGCCCGGTG GACGAGGAAG TCCCGCACCT CGTAGACCGT    240
GCACCAGCGC CCGGCGGCCC ACTCGGGGTC ACCCGCCCGC CACGGCCCGT CCCGGTGCTC    300
ACCGTGGGTG GTGCCCTCCG CGGCGAGGAG TTCGGTCCCG GTCAGAATCC AGTTGACGGA    360
CCACAGATGG TGGGTGATCG AGCGGATGGT GCCCCCGAGG TCGTCGAAGA GCCGGGCGAT    420
CTCGGACTTG CCCCGGGCCA GACCCCACTT GGGGAAGAAG AAGACCGCGT CCTCGGCGAA    480
GTAGTCGATC GCGGGGGTGC CGTCGCTGCC GACGCCGCCG TTGTCGAACG CCTTGAAGTA    540
CGCGGTGATG ACCGCCTTGC GCTGCTCGTC CGTCATACCG GCCGATGCCA CGGACATGAA    600
ACGACCTCCA GAGATTCCGG GTGGCTGTGC TGGGGCTGCG GAAGGGGTGT CCCCCGCGAA    660
GGACGGCGGA CGCCGCGGAC GCCGCGGCCG TCTCCCCGGC GGACGGGTCC CAGCGTCCTG    720
GAGAGGGCTT GGCGGCGGCT TGACGCCGTG CTGTCCCGCG GCTTGCGGAA CGCGAAGTAC    780
CGGCCAGCGT ACGGGCGTTG CACCGGACGT GTACGCCGGT CGGGACCCCT CGTACCCCCG    840
GAGCCGGCCG ACCCCGGCGG CTCCGGGGGT ACGGACGCGC CGGACCGGCC CGAGCGAGCC    900
GGACGGGTCG GACGGTGCGC GTGGTTCCGG TGTGTCGGAC AGCTCGGACG GACCGGACGG    960
TGCGCGTGGT TCCGGTGTGT CGGACAGCTC GGACGGGTCG GACGGTGCGC GTGGTTCCGG   1020
CACGCCGGAC GGGTCAGTTG CCGATCATGG CGAGCAATGC CGGGGTGTAC CGCTCCCCGG   1080
ACACCGGGTG GGAGATCGCG GCCGTCACCT CCGCGAGGGA CCGGTCGTCC AGCCGGATCG   1140
AGGCGGCGGC GAGATTGTCC GCGAGATGGG CCGGGTTCGC GGTGCCCGGG ATCGGGACGA   1200
CGTCCTCGCC CCGGTGGTGC AGCCAGGCGA GCGCGAGCTG TGCCAGGGTC AGCCCCAGAC   1260
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CGTCCGCGAC  CGGGCGCAGC  CGGTGCAGCA  ACGAGCGGTT  GCGCGCGAGG  GCCGGAGCGC  1320
TGAACCGGGG  CTGGCCCCGG  CGGAAGTCCT  CGTCCCCCAG  ATCGTCGGTG  GTGCGGATGG  1380
TGCCGGTGAG  AAAACCCCGT  CCCAGAGGGG  CGTAAGCGAC  GATCCCGATC  CCCAGCTCCC  1440
GGCAGACGGG  CACCACCTCG  TCCTCGATCC  CGCGCGACCA  CAGGCTCCAC  TCGCTCTGCA  1500
CCGCCGTCAC  CGGGTGCACC  GCGTCCGCCC  GGCGCAGCGT  GGCCGCGGAG  GGCTCGGAGA  1560
GACCGAGCCT  GCGGACCTTG  CCCTCGCGCA  CCAGCTCGGC  CACCGCACCC  ACGGTCTCCT  1620
CGATCGGCAC  CGCCGGGTCC  GTCCAGTGCT  GGTAGTACAG  GTCGATGCGG  TCGGTGCCGA  1680
GACGACGCAG  GGACCGTTCG  CAGGCCGCGC  GGACGTAGGA  CGGCTCGCCG  CACAAGCCCT  1740
GGGAGGCGCC  GTCGGACGAG  CGCACCATGC  CGAACTTGGT  GGCGATCAGC  ACCTCGTCCC  1800
GGCGGCCCGC  GACCGCCCGT  CCGAGCAGCT  CCTCACCGGC  GCCGAGCCCC  TGGACGTCGG  1860
CGGTGTCCAG  CAGGGTGACC  CCGGCGTCGA  CGGCGGCGCG  GATGGTGGCC  GTCGCCCGGG  1920
CGCGGTCCGG  GCGTCCGTAG  AAGTCGGTGG  TCGGCAGGCA  GCCGAGCCCC  TGGGCACTGA  1980
CCGGAAGGTC  CCGCAGGGCG  CGGACCGGCG  GACGCGGAAC  CGCGGCGGAC  ACGGAACCGG  2040
CCGGGGACTC  GGGCGGAGAG  CGGGACATAC  GGAACCTCCA  CAGGCGGAGC  CGGGAACGGG  2100
ACGAGGGCGA  GGACGGGACG  GAACGAAGGA  GAGGACGGGA  CGGACAGCAC  GGACGGGACG  2160
GACGGAACGG  AGTCGGGAAC  CGGGGGGGGT  GACCGGAACC  GGGCCGTCCT  TGGCCCTCCC  2220
CCGTCCTCCC  CGCCATCCGC  CGTTCTCCCC  CGTTCCCTCT  CCCGTCCTCC  AGCCAACACC  2280
GCCGCCCTTT  CCAAGCGCTT  GACACGGCAC  CGACAGCCGC  CGCCGGGCGC  CCGATGGGGA  2340
CCCGTGCCCG  CCGGTGAGCG  GCGGTGAGCG  CCGGTACGGG  ACCCCACGCG  CCGCCGCCCG  2400
GGCGCCCGCC  AGGGCCCGCG  CGGCCACCCC  GGCCCGCCCC  GGCCGGAGCG  GCGATCCGGG  2460
CCGCTCGCTG  CAAGAGGAAC  ATCCACAGCC  GCACAAGGAG  CGCTCCGCAC  AGTGGGCACC  2520
ACGTCCGCCC  CGTCCCCCAC  ACCGTGGCCG  GTCCCCACCG  GACAGCACAG  CACCGCACAG  2580
CACCACATCG  CACGGCACAG  CACAGCACCA  CCGGCACGAG  GAACCAAGGA  AAGGAACCAC  2640
ACCACCATGA  CCTCAGTGGA  CTGCACCGCG  TACGGCCCCG  AGCTGCGCGC  GCTCGCCGCC  2700
CGGCTGCCCC  GGACCCCCCG  GGCCGACCTG  TACGCCTTCC  TGGACGCCGC  GCACACAGCC  2760
GCCGCCTCGC  TCCCCGGCGC  CCTCGCCACC  GCGCTGGACA  CCTTCAACGC  CGAGGGCAGC  2820
GAGGACGGCC  ATCTGCTGCT  GCGCGGCCTC  CCGGTGGAGG  CCGACGCCGA  CCTCCCCACC  2880
ACCCCGAGCA  GCACCCCGGC  GCCCGAGGAC  CGCTCCCTGC  TGACCATGGA  GGCCATGCTC  2940
GGACTGGTGG  GCCGCCGGCT  CGGTCTGCAC  ACGGGGTACC  GGGAGCTGCG  CTCGGGCACG  3000
GTCTACCACG  ACGTGTACCC  GTCGCCCGGC  GCGCACCACC  TGTCCTCGGA  GACCTCCGAG  3060
ACGCTGCTGG  AGTTCCACAC  GGAGATGGCC  TACCACCGGC  TCCAGCCGAA  CTACGTCATG  3120
CTGGCCTGCT  CCCGGGCCGA  CCACGAGCGC  ACGGCGGCCA  CACTCGTCGC  CTCGGTCCGC  3180
AAGGCGCTGC  CCCTGCTGGA  CGAGAGGACC  CGGGCCCGGC  TCCTCGACCG  GAGGATGCCC  3240
TGCTGCGTGG  ATGTGGCCTT  CCGCGGCGGG  GTGGACGACC  CGGGCGCCAT  CGCCCAGGTC  3300
AAACCGCTCT  ACGGGGACGC  GGACGATCCC  TTCCTCGGGT  ACGACCGCGA  GCTGCTGGCG  3360
CCGGAGGACC  CCGCGGACAA  GGAGGCCGTC  GCCGCCCTGT  CCAAGGCGCT  CGACGAGGTC  3420
ACGGAGGCGG  TGTATCTGGA  GCCCGGCGAT  CTGCTGATCG  TCGACAACTT  CCGCACCACG  3480
CACGCGCGGA  CGCCGTTCTC  GCCCCGCTGG  GACGGGAAGG  ACCGCTGGCT  GCACCGCGTC  3540
TACATCCGCA  CCGACCGCAA  TGGACAGCTC  TCCGGCGGCG  AGCGCGCGGG  CGACGTCGTC  3600
GCCTTCACAC  CGCGCGGCTG  AGCTCCCGGG  TCCGACACCG  CGCGGCTGAA  CCCACGGTCC  3660
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GGGGCCCACG GTCCGGCACC GCGCGGCTGA GCCCCCGGGT CCGGCAGCGG GCGGCTGAAC    3720
CCCCGCCCCG GGCCACCGCC CGACCGCCCC CGCGCACCGG ACGCGCCCGC CTGTACGGCG    3780
GTCCCGCCCG GGCCCGTACA CCTGAAGCGC CCGGCGGACC GCCGCCCCGC CGGGGGACGG    3840
ACAGAGCCGG GTGCGGGAGG ACGTCCTCCC GCACCCGGCT CCCACCGTTC CGCACCGACC    3900
GCACCCGACC GTGCCGCAGG CGCCACCGGC ACCGCACCGC CCGCGCCGGC AGCCACCACA    3960
GGCGCCACGC CGCCCGCACG GTGCCCGCGC TGCTCAGCCC CCGTCCACCG GGCTGTCCAG    4020
CAGCCGCCGC AGCGCGCCCC CGATGAACTC CCGGTCGGCG GCCGACCCCC CGGACCCCGC    4080
GAGATGCCCC CACACTCCCG GGATCACCTC CAGCGAGGCA TACGGCAGCA GATCGGCCAC    4140
CCGCTTCTCG TCCTCGACGG CGAAACACAC GTCCAGGGCG CCCGGCAGCA CCACGGCCCG    4200
CGCCGTGACG GAGGCCAGCG CCGCCTCGAC GCTCCCCCCG GCCCCGGGTG TCGCCCCCAC    4260
ATCCGTGTTC TCCCAGGTGC GCACCATGGT GAGCAGATCC GCGGCGCCGG GCCCGGAGAG    4320
GAAGACCTGC TCCCAGAAGC CGGTGAGGTA CTCCTCGCGG GTGGCGAAAC CCAGCTCCCG    4380
GTGGGCACGG CGGGCCCAGA AGGAACGCGA GGTCCCCCAC CCGGCGAACA CCCGGCCCGC    4440
CGCCTTCCGC CCCCGCTCCC CGGCGTCGGC GCTGAGCGCC GCGGCCAGAC CGGACAGCAG    4500
GACCAGGCTG TGCGGGCTGC TCACCGGCGC CCCGCAGATC GGGGCGATCC GGCGCACCAT    4560
CCCCGGATGC GACACGGCCC ACTGGTAGGC GTGGGCCGCG CCCATCGACC AGCCCGTGAC    4620
CAGGGCCAGT TCCCGTACCC CCAGCTCCTC GGTGAGCAGC CGGTGCTGCG CCGCGACATT    4680
GTCCTGCGGA GTGATCAGCG GAAAGCGGGA CCCCGACGGG TGGTTGCCGG GCGAGCTGGA    4740
GACCCCGTTG CCGAAGAGTC CGGCGGTGAC GACGCAGTAC CGCCGGGTGT CCAGCGGCAG    4800
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CACCACGTTC GTCCCGTCGG CGTTCGGCGT GCCGTACATG GCGTAACCGA TCCGGGCGTC    4920
CCGCAGGACC TCCCCGTCCA GCAACGGCAG TTCGTCGATC TCGAATATGC GGCATTCCAC    4980
CGCTGACCTC CTTGTTCGAT CCCCCCGGAC AACAGGTCGG TCGTGGCCGG AGACTCAGAG    5040
CCAGTTGGGG GCGATCTCGG TGGCCCACAG CTCCAGGCTG CGCAGCTGGA CATCGTGCGG    5100
GATCAGCCCG GAGTACTGGC ACTGGAGCAG ATACTCCGGA TCGTGCCGCT CCACCAGCTT    5160
CTCGATCATG CGGTTGATGT CGTCCGGGGT GCCGACCCAC TCCAGCCCCC GGTCGACCAG    5220
GGTCTTGTAG TCCGAGCCGA TCGGACCCGT CTCGCCGGTC GCGCGCAGCG CCTCGGTGAA    5280
GCCCATGGGG CCGAACCAGT TCTCGAAGAT GAAGCCGCCG CCGCGGGACG CCCAGTGGTG    5340
GGCCTCGCCG GAGTCCCGGG AGACCAGGAC GTCCTTCATC ACCCCGACCC GCTCGCCCCG    5400
CCGCAGGGTG CCGTGGCCCG CCGCCTCGGC CTCCTCCCGG TAGATGTCCA TCAGCCGGGC    5460
GACGATCTGG TCGTCGGTGT TCATCAGGAT CGGCACCACG CCCTCCCGGG CACAGAACCG    5520
GAACGTGTCC TCACTGAAGC TGAACGGCTG GAAGACGGGC GGGTGGGGGC GCTGGTAGGG    5580
CTTGGGCGCG ATGCCCACCT CGCGGATGAC GCCGTTCTCG TCGAGGCCCC GGCCGTAGCG    5640
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GTGGGTGAAC GTCTCGGTCG TCCACGCCTT CTTGATGATC TCCCAGTGCT CCTCGAAGAG    5760
GGCACGATTG CGCCGGTCCC GCTCCCCGGC GTCGGACAGG GTGCCGCCGA CCCCGTACAC    5820
CTGCCCCATG ATGTCGGCCC AGCGCTTCTG GAACCCGCGC GCGATCCCGA CGAAGGCGCG    5880
GCCCCGGGTC ATGTGGTCGA GCATCGCCAG ATCCTCGGCC AGCCGCAGCG GATTGTGCAG    5940
CGGCAGGACG TTGGCCATCT GGCCGACCCG GATGTGCCGG GTCTGCATGC CGAGGTAGAG    6000
CCCCAGCATG ATCGGGTTGT TGGAGACCTC GAAACCCTCG GTGTGGAAGT GGTGCTCGGT    6060
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GAAGGACAGT CCCCAGTAGC CGAGTTCGTC GGCCGCCTGC GCCTGCCGGG TGAGCTGCCG    6120
GAGCATGTTC TGGTAGTTCT GCGGATTGAC CCCCGCCATA CCCCGCTGGA CCTGCGCATG    6180
ACTGCCGACC GTTGGCAGAT AGAAGAGAAT GGACTTCACC CTGGCTCCTC CGGTTCGCGG    6240
CGCCCTCCAT TGACGTGCGC CGAAAGCGGC TCGACCGTCC CACTCCGCCC TTGAGTTCCG    6300
TCTGACGCCG CGCCAGTCGG CGGGCCGTCC GCCGGGGTGC CCGCCGGGGT CCGCACCCGC    6360
CGGACGGCAC GGCGCGCACC GCGCGCGCGG CGCTTCGGGG CACCGGGCTC GACGGGGTGC    6420
TCAGCGGGAC GTCCAACGGA AGGCAAGCCC CCGTACCCAG CCTGGTCAAG GCGCTCATCG    6480
CCATTCCCTG AGGAGGTCCC GCCTTGACCA CAGCAATCTC CGCGCTCCCG ACCGTGCCCG    6540
GCTCCGGACT CGAAGCACTG GACCGTGCCA CCCTCATCCA CCCCACCCTC TCCGGAAACA    6600
CCGCGGAACG GATCGTGCTG ACCTCGGGGT CCGGCAGCCG GGTCCGCGAC ACCGACGGCC    6660
GGGAGTACCT GGACGCGAGC GCCGTCCTCG GGGTGACCCA GGTGGGCCAC GGCCGGGCCG    6720
AGCTGGCCCG GGTCGCGGCC GAGCAGATGG CCCGGCTGGA GTACTTCCAC ACCTGGGGGA    6780
CGATCAGCAA CGACCGGGCG GTGGAGCTGG CGGCACGGCT GGTGGGGCTG AGCCCGGAGC    6840
CGCTGACCCG CGTCTACTTC ACCAGCGGCG GGGCCGAGGG CAACGAGATC GCCCTGCGGA    6900
TGGCCCGGCT CTACCACCAC CGGCGCGGGG AGTCCGCCCG TACCTGGATA CTCTCCCGCC    6960
GGTCGGCCTA CCACGGCGTC GGATACGGCA GCGGCGGCGT CACCGGCTTC CCCGCCTACC    7020
ACCAGGGCTT CGGCCCCTCC CTCCCGGACG TCGACTTCCT GACCCCGCCG CAGCCCTACC    7080
GCCGGGAGCT GTTCGCCGGT TCCGACGTCA CCGACTTCTG CCTCGCCGAA CTGCGCGAGA    7140
CCATCGACCG GATCGGCCCG GAGCGGATCG CGGCGATGAT CGGCGAGCCG ATC           7193
```

        (2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 145 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Other

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GTGACCCGGC CTCCGGGCCT TTCCGCGCAC ACCCACGGGT CCGTGTCCGG GAGTCTGCTG      60
CGCCGGGTGG CGGGCCACTA TCCCACCGGG GTGGTCCTGG TCACCGGTCC GGCCGAGGCT     120
CCGGGGCAGC CGCCGCCCGC CATGG                                          145
```

        (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 453 base pairs

```
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: Other

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:3:
```

```
ATGTCCGTGG  CATCGGCCGG  TATGACGGAC  GAGCAGCGCA  AGGCGGTCAT  CACCGCGTAC     60
TTCAAGGCGT  TCGACAACGG  CGGCGTCGGC  AGCGACGGCA  CCCCCGCGAT  CGACTACTTC    120
GCCGAGGACG  CGGTCTTCTT  CTTCCCCAAG  TGGGGTCTGG  CCCGGGGCAA  GTCCGAGATC    180
GCCCGGCTCT  TCGACGACCT  CGGGGGCACC  ATCCGCTCGA  TCACCCACCA  TCTGTGGTCC    240
GTCAACTGGA  TTCTGACCGG  GACCGAACTC  CTCGCCGCGG  AGGGCACCAC  CCACGGTGAG    300
CACCGGGACG  GGCCGTGGCG  GGCGGGTGAC  CCCGAGTGGG  CCGCCGGGCG  CTGGTGCACG    360
GTCTACGAGG  TGCGGGACTT  CCTCGTCCAC  CGGGCCTTCG  TCTATCTGGA  CCCCGATTAC    420
GCGGGCAAGG  ACACCGCGCG  TTACCCGTGG  CTG                                   453
```

```
            (2)  INFORMATION FOR SEQ ID NO:4:

        (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 1032 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: Other

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:
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```
ATGTCCCGCT  CTCCGCCCGA  GTCCCCGGCC  GGTTCCGTGT  CCGCCGCGGT  TCCGCGTCCG     60
CCGGTCCGCG  CCCTGCGGGA  CCTTCCGGTC  AGTGCCCAGG  GGCTCGGCTG  CCTGCCGACC    120
ACCGACTTCT  ACGGACGCCC  GGACCGCGCC  CGGGCGACGG  CCACCATCCG  CGCCGCCGTC    180
GACGCCGGGG  TCACCCTGCT  GGACACCGCC  GACGTCCAGG  GGCTCGGCGC  CGGTGAGGAG    240
CTGCTCGGAC  GGGCGGTCGC  GGGCCGCCGG  GACGAGGTGC  TGATCGCCAC  CAAGTTCGGC    300
ATGGTGCGCT  CGTCCGACGG  CGCCTCCCAG  GGCTTGTGCG  GCGAGCCGTC  CTACGTCCGC    360
GCGGCCTGCG  AACGGTCCCT  GCGTCGTCTC  GGCACCGACC  GCATCGACCT  GTACTACCAG    420
CACTGGACGG  ACCCGGCGGT  GCCGATCGAG  GAGACCGTGG  GTGCGGTGGC  CGAGCTGGTG    480
CGCGAGGGCA  AGGTCCGCAG  GCTCGGTCTC  TCCGAGCCCT  CCGCGGCCAC  GCTGCGCCGG    540
GCGGACGCGG  TGCACCCGGT  GACGGCGGTG  CAGAGCGAGT  GGAGCCTGTG  GTCGCGCGGG    600
ATCGAGGACG  AGGTGGTGCC  CGTCTGCCGG  GAGCTGGGGA  TCGGGATCGT  CGCTTACGCC    660
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```
CCTCTGGGAC GGGGTTTTCT CACCGGCACC ATCCGCACCA CCGACGATCT GGGGGACGAG    720

GACTTCCGCC GGGGCCAGCC CCGGTTCAGC GCTCCGGCCC TCGCGCGCAA CCGCTCGTTG    780

CTGCACCGGC TGCGCCCGGT CGCGGACGGT CTGGGGCTGA CCCTGGCACA GCTCGCGCTC    840

GCCTGGCTGC ACCACCGGGG CGAGGACGTC GTCCCGATCC CGGGCACCGC GAACCCGGCC    900

CATCTCGCGG ACAATCTCGC CGCCGCCTCG ATCCGGCTGG ACGACCGGTC CCTCGCGGAG    960

GTGACGGCCG CGATCTCCCA CCCGGTGTCC GGGGAGCGGT ACACCCCGGC ATTGCTCGCC   1020

ATGATCGGCA AC                                                     1032
```

                    (2) INFORMATION FOR SEQ ID NO:5:

               (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 984 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear

               (ii) MOLECULE TYPE: Other

               (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
GTGGAATGCC GCATATTCGA GATCGACGAA CTGCCGTTGC TGGACGGGGA GGTCCTGCGG     60

GACGCCCGGA TCGGTTACGC CATGTACGGC ACGCCGAACG CCGACGGGAC GAACGTGGTG    120

CTCTGTCCGT CGTTCTTCGG CCGGGACCAC ACCGGGTACG ACTGGCTGAT CGGTGCGGGG    180

CTGCCGCTGG ACACCCGGCG GTACTGCGTC GTCACCGCCG GACTCTTCGG CAACGGGGTC    240

TCCAGCTCGC CCGGCAACCA CCCGTCGGGG TCCCGCTTTC CGCTGATCAC TCCGCAGGAC    300

AATGTCGCGG CGCAGCACCG GCTGCTCACC GAGGAGCTGG GGTACGGGA ACTGGCCCTG     360

GTCACGGGCT GGTCGATGGG CGCGGCCCAC GCCTACCAGT GGGCCGTGTC GCATCCGGGG    420

ATGGTGCGCC GGATCGCCCC GATCTGCGGG GCGCCGGTGA GCAGCCCGCA CAGCCTGGTC    480

CTGCTGTCCG GTCTGGCCGC GGCGCTCAGC GCCGACGCCG GGGAGCGGGG GCGGAAGGCG    540

GCGGGCCGGG TGTTCGCCGG GTGGGGGACC TCGCGTTCCT TCTGGGCCCG CCGTGCCCAC    600

CGGGAGCTGG GTTTCGCCAC CCGCGAGGAG TACCTCACCG GCTTCTGGGA GCAGGTCTTC    660

CTCTCCGGGC CCGGCGCCGC GGATCTGCTC ACCATGGTGC GCACCTGGGA GAACACGGAT    720

GTGGGGGCGA CACCCGGGGC CGGGGGGAGC GTCGAGGCGG CGCTGGCCTC CGTCACGGCG    780

CGGGCCGTGG TGCTGCCGGG CGCCCTGGAC GTGTGTTTCG CCGTCGAGGA CGAGAAGCGG    840

GTGGCCGATC TGCTGCCGTA TGCCTCGCTG GAGGTGATCC CGGGAGTGTG GGGGCATCTC    900

GCGGGGTCCG GGGGGTCGGC CGCCGACCGG GAGTTCATCG GGGGCGCGCT GCGGCGGCTG    960

CTGGACAGCC CGGTGGACGG GGGC                                          984
```

                (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1182 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GTGAAGTCCA TTCTCTTCTA TCTGCCAACG GTCGGCAGTC ATGCGCAGGT CCAGCGGGGT      60
ATGGCGGGGG TCAATCCGCA GAACTACCAG AACATGCTCC GGCAGCTCAC CCGGCAGGCG     120
CAGGCGGCCG ACGAACTCGG CTACTGGGGA CTGTCCTTCA CCGAGCACCA CTTCCACACC     180
GAGGGTTTCG AGGTCTCCAA CAACCCGATC ATGCTGGGGC TCTACCTCGG CATGCAGACC     240
CGGCACATCC GGGTCGGCCA GATGGCCAAC GTCCTGCCGC TGCACAATCC GCTGCGGCTG     300
GCCGAGGATC TGGCGATGCT CGACCACATG ACCCGGGGCC GCGCCTTCGT CGGGATCGCG     360
CGCGGGTTCC AGAAGCGCTG GGCCGACATC ATGGGGCAGG TGTACGGGGT CGGCGGCACC     420
CTGTCCGACG CCGGGGAGCG GGACCGGCGC AATCGTGCCC TCTTCGAGGA GCACTGGGAG     480
ATCATCAAGA AGGCGTGGAC GACCGAGACG TTCACCCACT CCGGGGAGCA GTGGACGATC     540
CCGGTGCCGG ACCTGGAGTT CCCCTACGAG GCGGTGCGCC GCTACGGCCG GGGCCTCGAC     600
GAGAACGGCG TCATCCGCGA GGTGGGCATC GCGCCCAAGC CCTACCAGCG CCCCCACCCG     660
CCCGTCTTCC AGCCGTTCAG CTTCAGTGAG GACACGTTCC GGTTCTGTGC CCGGGAGGGC     720
GTGGTGCCGA TCCTGATGAA CACCGACGAC CAGATCGTCG CCCGGCTGAT GGACATCTAC     780
CGGGAGGAGG CCGAGGCGGC GGGCCACGGC ACCCTGCGGC GGGGCGAGCG GGTCGGGGTG     840
ATGAAGGACG TCCTGGTCTC CCGGGACTCC GGCGAGGCCC ACCACTGGGC GTCCCGCGGC     900
GGCGGCTTCA TCTTCGAGAA CTGGTTCGGC CCCATGGGCT TCACCGAGGC GCTGCGCGCG     960
ACCGGCGAGA CGGGTCCGAT CGGCTCGGAC TACAAGACCC TGGTCGACCG GGGGCTGGAG    1020
TGGGTCGGCA CCCCGGACGA CATCAACCGC ATGATCGAGA AGCTGGTGGA GCGGCACGAT    1080
CCGGAGTATC TGCTCCAGTG CCAGTACTCC GGGCTGATCC CGCACGATGT CCAGCTGCGC    1140
AGCCTGGAGC TGTGGGCCAC CGAGATCGCC CCCAACTGGC TC                       1182
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 660 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GTGCCCGGCT  CCGGACTCGA  AGCACTGGAC  CGTGCCACCC  TCATCCACCC  CACCCTCTCC      60
GGAAACACCG  CGGAACGGAT  CGTGCTGACC  TCGGGGTCCG  GCAGCCGGGT  CCGCGACACC     120
GACGGCCGGG  AGTACCTGGA  CGCGAGCGCC  GTCCTCGGGG  TGACCCAGGT  GGGCCACGGC     180
CGGGCCGAGC  TGGCCCGGGT  CGCGGCCGAG  CAGATGGCCC  GGCTGGAGTA  CTTCCACACC     240
TGGGGGACGA  TCAGCAACGA  CCGGGCGGTG  GAGCTGGCGG  CACGGCTGGT  GGGGCTGAGC     300
CCGGAGCCGC  TGACCCGCGT  CTACTTCACC  AGCGGCGGGG  CCGAGGGCAA  CGAGATCGCC     360
CTGCGGATGG  CCCGGCTCTA  CCACCACCGG  CGCGGGGAGT  CCGCCCGTAC  CTGGATACTC     420
TCCCGCCGGT  CGGCCTACCA  CGGCGTCGGA  TACGGCAGCG  GCGGCGTCAC  CGGCTTCCCC     480
GCCTACCACC  AGGGCTTCGG  CCCCTCCCTC  CCGGACGTCG  ACTTCCTGAC  CCCGCCGCAG     540
CCCTACCGCC  GGGAGCTGTT  CGCCGGTTCC  GACGTCACCG  ACTTCTGCCT  CGCCGAACTG     600
CGCGAGACCA  TCGACCGGAT  CGGCCCGGAG  CGGATCGCGG  CGATGATCGG  CGAGCCGATC     660
```

        (2) INFORMATION FOR SEQ ID NO:8:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Other

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
CTGACGCTGC  AGGAGGAAGT  CCCGC                                                25
```

        (2) INFORMATION FOR SEQ ID NO:9:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Other

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGGCGAGG ACGTCGTCCC GATCC   25

       (2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 25 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCCCCTGG ACGTCGGCGG TGTCC   25

       (2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 25 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GACGGTGCAT GCTCAGCAGG GAGCG   25

       (2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 972 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
ATGACCTCAG TGGACTGCAC CGCGTACGGC CCCGAGCTGC GCGCGCTCGC CGCCCGGCTG          60
CCCCGGACCC CCCGGGCCGA CCTGTACGCC TTCCTGGACG CCGCGCACAC AGCCGCCGCC         120
TCGCTCCCCG CGCCCCTCGC CACCGCGCTG GACACCTTCA ACGCCGAGGG CAGCGAGGAC         180
GGCCATCTGC TGCTGCGCGG CCTCCCGGTG GAGGCCGACG CCGACCTCCC CACCACCCCG         240
AGCAGCACCC CGGCGCCCGA GGACCGCTCC CTGCTGACCA TGGAGGCCAT GCTCGGACTG         300
GTGGGCCGCC GGCTCGGTCT GCACACGGGG TACCGGGAGC TGCGCTCGGG CACGGTCTAC         360
CACGACGTGT ACCCGTCGCC CGGCGCGCAC CACCTGTCCT CGGAGACCTC CGAGACGCTG         420
CTGGAGTTCC ACACGGAGAT GGCCTACCAC CGGCTCCAGC CGAACTACGT CATGCTGGCC         480
TGCTCCCGGG CCGACCACGA GCGCACGGCG GCCACACTCG TCGCCTCGGT CCGCAAGGCG         540
CTGCCCCTGC TGGACGAGAG GACCCGGGCC CGGCTCCTCG ACCGGAGGAT GCCCTGCTGC         600
GTGGATGTGG CCTTCCGCGG CGGGGTGGAC GACCCGGGCG CCATCGCCCA GGTCAAACCG         660
CTCTACGGGG ACGCGGACGA TCCCTTCCTC GGGTACGACC GCGAGCTGCT GGCGCCGGAG         720
GACCCCGCGG ACAAGGAGGC CGTCGCCGCC CTGTCCAAGG CGCTCGACGA GGTCACGGAG         780
GCGGTGTATC TGGAGCCCGG CGATCTGCTG ATCGTCGACA ACTTCCGCAC CACGCACGCG         840
CGGACGCCGT TCTCGCCCCG CTGGGACGGG AAGGACCGCT GGCTGCACCG CGTCTACATC         900
CGCACCGACC GCAATGGACA GCTCTCCGGC GGCGAGCGCG CGGGCGACGT CGTCGCCTTC         960
ACACCGCGCG GC                                                            972
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 48 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Thr Arg Pro Pro Gly Leu Ser Ala His Thr His Gly Ser Val Ser
1               5                   10                  15
Gly Ser Leu Leu Arg Arg Val Ala Gly His Tyr Pro Thr Gly Val Val
                20                  25                  30
Leu Val Thr Gly Pro Ala Glu Ala Pro Gly Gln Pro Pro Pro Ala Met
                35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 151 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Ser Val Ala Ser Ala Gly Met Thr Asp Glu Gln Arg Lys Ala Val
1               5                   10                  15
Ile Thr Ala Tyr Phe Lys Ala Phe Asp Asn Gly Gly Val Gly Ser Asp
                20                  25                  30
Gly Thr Pro Ala Ile Asp Tyr Phe Ala Glu Asp Ala Val Phe Phe Phe
            35                  40                  45
Pro Lys Trp Gly Leu Ala Arg Gly Lys Ser Glu Ile Ala Arg Leu Phe
    50                  55                  60
Asp Asp Leu Gly Gly Thr Ile Arg Ser Ile Thr His His Leu Trp Ser
65                  70                  75                  80
Val Asn Trp Ile Leu Thr Gly Thr Glu Leu Leu Ala Ala Glu Gly Thr
                85                  90                  95
Thr His Gly Glu His Arg Asp Gly Pro Trp Arg Ala Gly Asp Pro Glu
            100                 105                 110
Trp Ala Ala Gly Arg Trp Cys Thr Val Tyr Glu Val Arg Asp Phe Leu
            115                 120                 125
Val His Arg Ala Phe Val Tyr Leu Asp Pro Asp Tyr Ala Gly Lys Asp
    130                 135                 140
Thr Ala Arg Tyr Pro Trp Leu
145                 150
```

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 344 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

```
      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ser Arg Ser Pro Pro Glu Ser Pro Ala Gly Ser Val Ser Ala Ala
 1               5                  10                  15
Val Pro Arg Pro Pro Val Arg Ala Leu Arg Asp Leu Pro Val Ser Ala
            20                  25                  30
Gln Gly Leu Gly Cys Leu Pro Thr Thr Asp Phe Tyr Gly Arg Pro Asp
        35                  40                  45
Arg Ala Arg Ala Thr Ala Thr Ile Arg Ala Ala Val Asp Ala Gly Val
        50                  55                  60
Thr Leu Leu Asp Thr Ala Asp Val Gln Gly Leu Gly Ala Gly Glu Glu
65                  70                  75                  80
Leu Leu Gly Arg Ala Val Ala Gly Arg Arg Asp Glu Val Leu Ile Ala
                85                  90                  95
Thr Lys Phe Gly Met Val Arg Ser Ser Asp Gly Ala Ser Gln Gly Leu
               100                 105                 110
Cys Gly Glu Pro Ser Tyr Val Arg Ala Ala Cys Glu Arg Ser Leu Arg
        115                 120                 125
Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Tyr Gln His Trp Thr Asp
        130                 135                 140
Pro Ala Val Pro Ile Glu Glu Thr Val Gly Ala Val Ala Glu Leu Val
145                 150                 155                 160
Arg Glu Gly Lys Val Arg Arg Leu Gly Leu Ser Glu Pro Ser Ala Ala
               165                 170                 175
Thr Leu Arg Arg Ala Asp Ala Val His Pro Val Thr Ala Val Gln Ser
               180                 185                 190
Glu Trp Ser Leu Trp Ser Arg Gly Ile Glu Asp Glu Val Val Pro Val
        195                 200                 205
Cys Arg Glu Leu Gly Ile Gly Ile Val Ala Tyr Ala Pro Leu Gly Arg
        210                 215                 220
Gly Phe Leu Thr Gly Thr Ile Arg Thr Thr Asp Asp Leu Gly Asp Glu
225                 230                 235                 240
Asp Phe Arg Arg Gly Gln Pro Arg Phe Ser Ala Pro Ala Leu Ala Arg
               245                 250                 255
Asn Arg Ser Leu Leu His Arg Leu Arg Pro Val Ala Asp Gly Leu Gly
               260                 265                 270
Leu Thr Leu Ala Gln Leu Ala Leu Ala Trp Leu His His Arg Gly Glu
```

```
        275                    280                    285
Asp Val Val Pro Ile Pro Gly Thr Ala Asn Pro Ala His Leu Ala Asp
        290                    295                    300
Asn Leu Ala Ala Ala Ser Ile Arg Leu Asp Asp Arg Ser Leu Ala Glu
305                    310                    315                    320
Val Thr Ala Ala Ile Ser His Pro Val Ser Gly Glu Arg Tyr Thr Pro
                       325                    330                    335
Ala Leu Leu Ala Met Ile Gly Asn
                       340
```

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 328 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Glu Cys Arg Ile Phe Glu Ile Asp Glu Leu Pro Leu Leu Asp Gly
1                   5                   10                  15
Glu Val Leu Arg Asp Ala Arg Ile Gly Tyr Ala Met Tyr Gly Thr Pro
            20                  25                  30
Asn Ala Asp Gly Thr Asn Val Val Leu Cys Pro Ser Phe Phe Gly Arg
            35                  40                  45
Asp His Thr Gly Tyr Asp Trp Leu Ile Gly Ala Gly Leu Pro Leu Asp
            50                  55                  60
Thr Arg Arg Tyr Cys Val Val Thr Ala Gly Leu Phe Gly Asn Gly Val
65                  70                  75                  80
Ser Ser Ser Pro Gly Asn His Pro Ser Gly Ser Arg Phe Pro Leu Ile
                  85                  90                  95
Thr Pro Gln Asp Asn Val Ala Ala Gln His Arg Leu Leu Thr Glu Glu
                  100                 105                 110
Leu Gly Val Arg Glu Leu Ala Leu Val Thr Gly Trp Ser Met Gly Ala
            115                 120                 125
Ala His Ala Tyr Gln Trp Ala Val Ser His Pro Gly Met Val Arg Arg
            130                 135                 140
```

```
Ile Ala Pro Ile Cys Gly Ala Pro Val Ser Ser Pro His Ser Leu Val
145             150             155                 160

Leu Leu Ser Gly Leu Ala Ala Ala Leu Ser Ala Asp Ala Gly Glu Arg
                165             170             175

Gly Arg Lys Ala Ala Gly Arg Val Phe Ala Gly Trp Gly Thr Ser Arg
            180             185             190

Ser Phe Trp Ala Arg Arg Ala His Arg Glu Leu Gly Phe Ala Thr Arg
            195             200             205

Glu Glu Tyr Leu Thr Gly Phe Trp Glu Gln Val Phe Leu Ser Gly Pro
    210             215             220

Gly Ala Ala Asp Leu Leu Thr Met Val Arg Thr Trp Glu Asn Thr Asp
225             230             235             240

Val Gly Ala Thr Pro Gly Ala Gly Gly Ser Val Glu Ala Ala Leu Ala
            245             250             255

Ser Val Thr Ala Arg Ala Val Val Leu Pro Gly Ala Leu Asp Val Cys
            260             265             270

Phe Ala Val Glu Asp Glu Lys Arg Val Ala Asp Leu Leu Pro Tyr Ala
        275             280             285

Ser Leu Glu Val Ile Pro Gly Val Trp Gly His Leu Ala Gly Ser Gly
    290             295             300

Gly Ser Ala Ala Asp Arg Glu Phe Ile Gly Gly Ala Leu Arg Arg Leu
305             310             315             320

Leu Asp Ser Pro Val Asp Gly Gly
            325
```

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 394 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Met Lys Ser Ile Leu Phe Tyr Leu Pro Thr Val Gly Ser His Ala Gln
1               5               10              15

Val Gln Arg Gly Met Ala Gly Val Asn Pro Gln Asn Tyr Gln Asn Met
```

```
                 20                      25                      30
     Leu Arg Gln Leu Thr Arg Gln Ala Gln Ala Ala Asp Glu Leu Gly Tyr
             35                      40                      45
     Trp Gly Leu Ser Phe Thr Glu His His Phe His Thr Glu Gly Phe Glu
         50                      55                      60
     Val Ser Asn Asn Pro Ile Met Leu Gly Leu Tyr Leu Gly Met Gln Thr
     65                      70                      75                      80
     Arg His Ile Arg Val Gly Gln Met Ala Asn Val Leu Pro Leu His Asn
                         85                      90                      95
     Pro Leu Arg Leu Ala Glu Asp Leu Ala Met Leu Asp His Met Thr Arg
                 100                     105                     110
     Gly Arg Ala Phe Val Gly Ile Ala Arg Gly Phe Gln Lys Arg Trp Ala
             115                     120                     125
     Asp Ile Met Gly Gln Val Tyr Gly Val Gly Gly Thr Leu Ser Asp Ala
             130                     135                     140
     Gly Glu Arg Asp Arg Arg Asn Arg Ala Leu Phe Glu Glu His Trp Glu
     145                     150                     155                     160
     Ile Ile Lys Lys Ala Trp Thr Thr Glu Thr Phe Thr His Ser Gly Glu
                 165                     170                     175
     Gln Trp Thr Ile Pro Val Pro Asp Leu Glu Phe Pro Tyr Glu Ala Val
                 180                     185                     190
     Arg Arg Tyr Gly Arg Gly Leu Asp Glu Asn Gly Val Ile Arg Glu Val
             195                     200                     205
     Gly Ile Ala Pro Lys Pro Tyr Gln Arg Pro His Pro Pro Val Phe Gln
             210                     215                     220
     Pro Phe Ser Phe Ser Glu Asp Thr Phe Arg Phe Cys Ala Arg Glu Gly
     225                     230                     235                     240
     Val Val Pro Ile Leu Met Asn Thr Asp Asp Gln Ile Val Ala Arg Leu
                 245                     250                     255
     Met Asp Ile Tyr Arg Glu Glu Ala Glu Ala Ala Gly His Gly Thr Leu
                 260                     265                     270
     Arg Arg Gly Glu Arg Val Gly Val Met Lys Asp Val Leu Val Ser Arg
             275                     280                     285
     Asp Ser Gly Glu Ala His His Trp Ala Ser Arg Gly Gly Gly Phe Ile
             290                     295                     300
     Phe Glu Asn Trp Phe Gly Pro Met Gly Phe Thr Glu Ala Leu Arg Ala
     305                     310                     315                     320
     Thr Gly Glu Thr Gly Pro Ile Gly Ser Asp Tyr Lys Thr Leu Val Asp
                 325                     330                     335
     Arg Gly Leu Glu Trp Val Gly Thr Pro Asp Asp Ile Asn Arg Met Ile
```

```
                340                    345                    350
Glu Lys Leu Val Glu Arg His Asp Pro Glu Tyr Leu Leu Gln Cys Gln
        355                    360                    365
Tyr Ser Gly Leu Ile Pro His Asp Val Gln Leu Arg Ser Leu Glu Leu
    370                    375                    380
Trp Ala Thr Glu Ile Ala Pro Asn Trp Leu
385                    390
```

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 220 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Pro Gly Ser Gly Leu Glu Ala Leu Asp Arg Ala Thr Leu Ile His
1                   5                   10                  15
Pro Thr Leu Ser Gly Asn Thr Ala Glu Arg Ile Val Leu Thr Ser Gly
                20                  25                  30
Ser Gly Ser Arg Val Arg Asp Thr Asp Gly Arg Glu Tyr Leu Asp Ala
        35                  40                  45
Ser Ala Val Leu Gly Val Thr Gln Val Gly His Gly Arg Ala Glu Leu
    50                  55                  60
Ala Arg Val Ala Ala Glu Gln Met Ala Arg Leu Glu Tyr Phe His Thr
65                  70                  75                  80
Trp Gly Thr Ile Ser Asn Asp Arg Ala Val Glu Leu Ala Ala Arg Leu
                85                  90                  95
Val Gly Leu Ser Pro Glu Pro Leu Thr Arg Val Tyr Phe Thr Ser Gly
                100                 105                 110
Gly Ala Glu Gly Asn Glu Ile Ala Leu Arg Met Ala Arg Leu Tyr His
            115                 120                 125
His Arg Arg Gly Glu Ser Ala Arg Thr Trp Ile Leu Ser Arg Arg Ser .
        130                 135                 140
Ala Tyr His Gly Val Gly Tyr Gly Ser Gly Gly Val Thr Gly Phe Pro
145                 150                 155                 160
```

```
Ala Tyr His Gln Gly Phe Gly Pro Ser Leu Pro Asp Val Asp Phe Leu
            165             170             175
Thr Pro Pro Gln Pro Tyr Arg Arg Glu Leu Phe Ala Gly Ser Asp Val
            180             185             190
Thr Asp Phe Cys Leu Ala Glu Leu Arg Glu Thr Ile Asp Arg Ile Gly
        195             200             205
Pro Glu Arg Ile Ala Ala Met Ile Gly Glu Pro Ile
210             215             220
```

        (2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 324 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Thr Ser Val Asp Cys Thr Ala Tyr Gly Pro Glu Leu Arg Ala Leu
1               5               10              15
Ala Ala Arg Leu Pro Arg Thr Pro Arg Ala Asp Leu Tyr Ala Phe Leu
            20              25              30
Asp Ala Ala His Thr Ala Ala Ala Ser Leu Pro Gly Ala Leu Ala Thr
            35              40              45
Ala Leu Asp Thr Phe Asn Ala Glu Gly Ser Glu Asp Gly His Leu Leu
        50              55              60
Leu Arg Gly Leu Pro Val Glu Ala Asp Ala Asp Leu Pro Thr Thr Pro
65              70              75              80
Ser Ser Thr Pro Ala Pro Glu Asp Arg Ser Leu Leu Thr Met Glu Ala
            85              90              95
Met Leu Gly Leu Val Gly Arg Arg Leu Gly Leu His Thr Gly Tyr Arg
            100             105             110
Glu Leu Arg Ser Gly Thr Val Tyr His Asp Val Tyr Pro Ser Pro Gly
        115             120             125
Ala His His Leu Ser Ser Glu Thr Ser Glu Thr Leu Leu Glu Phe His
        130             135             140
Thr Glu Met Ala Tyr His Arg Leu Gln Pro Asn Tyr Val Met Leu Ala
```

```
145                    150                    155                    160
Cys Ser Arg Ala Asp His Glu Arg Thr Ala Ala Thr Leu Val Ala Ser
                    165                    170                    175
Val Arg Lys Ala Leu Pro Leu Leu Asp Glu Arg Thr Arg Ala Arg Leu
                    180                    185                    190
Leu Asp Arg Arg Met Pro Cys Cys Val Asp Val Ala Phe Arg Gly Gly
          195                    200                    205
Val Asp Asp Pro Gly Ala Ile Ala Gln Val Lys Pro Leu Tyr Gly Asp
          210                    215                    220
Ala Asp Asp Pro Phe Leu Gly Tyr Asp Arg Glu Leu Leu Ala Pro Glu
225                    230                    235                    240
Asp Pro Ala Asp Lys Glu Ala Val Ala Ala Leu Ser Lys Ala Leu Asp
                    245                    250                    255
Glu Val Thr Glu Ala Val Tyr Leu Glu Pro Gly Asp Leu Leu Ile Val
                    260                    265                    270
Asp Asn Phe Arg Thr Thr His Ala Arg Thr Pro Phe Ser Pro Arg Trp
          275                    280                    285
Asp Gly Lys Asp Arg Trp Leu His Arg Val Tyr Ile Arg Thr Asp Arg
          290                    295                    300
Asn Gly Gln Leu Ser Gly Gly Glu Arg Ala Gly Asp Val Val Ala Phe
305                    310                    315                    320
Thr Pro Arg Gly
```